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Sequence Listing was accepted.

See attached Validation Report.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=12; day=4; hr=7; min=24; sec=12; ms=815;]

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Application No: 09540245 Version No: 2.0

Input Set:

Output Set:

Started: 2008-12-02 10:18:59.302
Finished: 2008-12-02 10:19:02.950
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 648 ms
Total Warnings: 14
Total Errors: 1
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
E 341	'Xaa' position not defined SEQID (5) POS (153)
W 402	Undefined organism found in <213> in SEQ ID (6)
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W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

<110> APPLICANT: Goodman, Corey
Kid, Thomas
Brose, Katja
Tessier-Lavigne, Marc
<120> TITLE OF INVENTION: Modulating Robo: Ligand Interactions
<130> FILE REFERENCE: B98-031-3

<140> CURRENT APPLICATION NUMBER:09540245
<141> CURRENT FILING DATE:2000-03-31
<150> PRIOR APPLICATION NUMBER: 60/065,544
<151> PRIOR FILING DATE: 1997-11-14
<150> PRIOR APPLICATION NUMBER: 60/081,057
<151> PRIOR FILING DATE: 1998-04-07
<160> NUMBER OF SEQ ID NOS: 20
<170> SOFTWARE: PatentIn Ver. 2.0

<210> SEQ ID NO 1

<211> LENGTH: 4758

<212> TYPE: DNA

<213> ORGANISM: human

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(4575)

<400> SEQUENCE: 1

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1 5 10 15	
ctg gcg atc ctg aac aag gtg gca ccg cag gcg tgc ccg gcg cag tgc	96
Leu Ala Ile Leu Asn Lys Val Ala Pro Gln Ala Cys Pro Ala Gln Cys	
20 25 30	
tct tgc tcg ggc agc aca gtg gac tgt cac ggg ctg gcg ctg cgc agc	144
Ser Cys Ser Gly Ser Thr Val Asp Cys His Gly Leu Ala Leu Arg Ser	
35 40 45	
gtg ccc agg aat atc ccc cgc aac acc gag aga ctg gat tta aat gga	192
Val Pro Arg Asn Ile Pro Arg Asn Thr Glu Arg Leu Asp Leu Asn Gly	
50 55 60	
aat aac atc aca aga att acg aag aca gat ttt gct ggt ctt aga cat	240
Asn Asn Ile Thr Arg Ile Thr Lys Thr Asp Phe Ala Gly Leu Arg His	
65 70 75 80	
cta aga gtt ctt cag ctt atg gag aat aag att agc acc att gaa aga	288
Leu Arg Val Leu Gln Leu Met Glu Asn Lys Ile Ser Thr Ile Glu Arg	
85 90 95	
gga gca ttc cag gat ctt aaa gaa cta gag aga ctg cgt tta aac aga	336
Gly Ala Phe Gln Asp Leu Lys Glu Leu Glu Arg Leu Arg Leu Asn Arg	
100 105 110	
aat cac ctt cag ctg ttt cct gag ttg ctg ttt ctt ggg act gcg aag	384
Asn His Leu Gln Leu Phe Pro Glu Leu Leu Phe Leu Gly Thr Ala Lys	
115 120 125	
cta tac agg ctt gat ctc agt gaa aac caa att cag gca atc cca agg	432
Leu Tyr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Ala Ile Pro Arg	
130 135 140	
aaa gct ttc cgt ggg gca gtt gac ata aaa aat ttg caa ctg gat tac	480
Lys Ala Phe Arg Gly Ala Val Asp Ile Lys Asn Leu Gln Leu Asp Tyr	
145 150 155 160	
aac cag atc agc tgt att gaa gat ggg gca ttc agg gct ctc cgg gac	528
Asn Gln Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu Arg Asp	
165 170 175	

ctg gaa gtg ctc act ctc aac aat aac aac att act aga ctt tct gtg	576		
Leu Glu Val Leu Thr Leu Asn Asn Asn Asn Ile Thr Arg Leu Ser Val			
180	185	190	
gca agt ttc aac cat atg cct aaa ctt agg act ttt cga ctg cat tca	624		
Ala Ser Phe Asn His Met Pro Lys Leu Arg Thr Phe Arg Leu His Ser			
195	200	205	
aac aac ctg tat tgt gac tgc cac ctg gcc tgg ctc tcc gac tgg ctt	672		
Asn Asn Leu Tyr Cys Asp Cys His Leu Ala Trp Leu Ser Asp Trp Leu			
210	215	220	
cgc aaa agg cct cgg gtt ggt ctg tac act cag tgt atg ggc ccc tcc	720		
Arg Lys Arg Pro Arg Val Gly Leu Tyr Thr Gln Cys Met Gly Pro Ser			
225	230	235	240
cac ctg aga ggc cat aat gta gcc gag gtt caa aaa cga gaa ttt gtc	768		
His Leu Arg Gly His Asn Val Ala Glu Val Gln Lys Arg Glu Phe Val			
245	250	255	
tgc agt gat gag gaa gaa ggt cac cag tca ttt atg gct cct tct tgt	816		
Cys Ser Asp Glu Glu Gly His Gln Ser Phe Met Ala Pro Ser Cys			
260	265	270	
agt gtt ttg cac tgc cct gcc gcc tgt acc tgt agc aac aat atc gta	864		
Ser Val Leu His Cys Pro Ala Ala Cys Thr Cys Ser Asn Asn Ile Val			
275	280	285	
gac tgt cgt ggg aaa ggt ctc act gag atc ccc aca aat ctt cca gag	912		
Asp Cys Arg Gly Lys Gly Leu Thr Glu Ile Pro Thr Asn Leu Pro Glu			
290	295	300	
acc atc aca gaa ata cgt ttg gaa cag aac aca atc aaa gtc atc cct	960		
Thr Ile Thr Glu Ile Arg Leu Glu Gln Asn Thr Ile Lys Val Ile Pro			
305	310	315	320
cct gga gct ttc tca cca tat aaa aag ctt aga cga att gac ctg agc	1008		
Pro Gly Ala Phe Ser Pro Tyr Lys Lys Leu Arg Arg Ile Asp Leu Ser			
325	330	335	
aat aat cag atc tct gaa ctt gca cca gat gct ttc caa gga cta cgc	1056		
Asn Asn Gln Ile Ser Glu Leu Ala Pro Asp Ala Phe Gln Gly Leu Arg			
340	345	350	
tct ctg aat tca ctt gtc ctc tat gga aat aaa atc aca gaa ctc ccc	1104		
Ser Leu Asn Ser Leu Val Leu Tyr Gly Asn Lys Ile Thr Glu Leu Pro			
355	360	365	
aaa agt tta ttt gaa gga ctg ttt tcc tta cag ctc cta tta ttg aat	1152		
Lys Ser Leu Phe Glu Gly Leu Phe Ser Leu Gln Leu Leu Leu Asn			
370	375	380	
gcc aac aag ata aac tgc ctt cgg gta gat gct ttt cag gat ctc cac	1200		
Ala Asn Lys Ile Asn Cys Leu Arg Val Asp Ala Phe Gln Asp Leu His			
385	390	395	400
aac ttg aac ctt ctc tcc cta tat gac aac aag ctt cag acc atc gcc	1248		
Asn Leu Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ala			
405	410	415	
aag ggg acc ttt tca cct ctt cgg gcc att caa act atg cat ttg gcc	1296		
Lys Gly Thr Phe Ser Pro Leu Arg Ala Ile Gln Thr Met His Leu Ala			
420	425	430	
cag aac ccc ttt att tgt gac tgc cat ctc aag tgg cta gcg gat tat	1344		
Gln Asn Pro Phe Ile Cys Asp Cys His Leu Lys Trp Leu Ala Asp Tyr			
435	440	445	
ctc cat acc aac ccg att gag acc agt ggt gcc cgt tgc acc agc ccc	1392		
Leu His Thr Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Thr Ser Pro			
450	455	460	
cgc cgc ctg gca aac aaa aga att gga cag atc aaa agc aag aaa ttc	1440		
Arg Arg Leu Ala Asn Lys Arg Ile Gly Gln Ile Lys Ser Lys Lys Phe			
465	470	475	480

cgt tgt tca ggt aca gaa gat tat cga tca aaa tta agt gga gac tgc	485	490	495	1488
Arg Cys Ser Gly Thr Glu Asp Tyr Arg Ser Lys Leu Ser Gly Asp Cys				
ttt gcg gat ctg gct tgc cct gaa aag tgt cgc tgt gaa gga acc aca	500	505	510	1536
Phe Ala Asp Leu Ala Cys Pro Glu Lys Cys Arg Cys Glu Gly Thr Thr				
gta gat tgc tct aat caa aag ctc aac aaa atc ccg gag cac att ccc	515	520	525	1584
Val Asp Cys Ser Asn Gln Lys Leu Asn Lys Ile Pro Glu His Ile Pro				
cag tac act gca gag ttg cgt ctc aat aat gaa ttt acc gtg ttg	530	535	540	1632
Gln Tyr Thr Ala Glu Leu Arg Leu Asn Asn Asn Glu Phe Thr Val Leu				
gaa gcc aca gga atc ttt aag aaa ctt cct caa tta cgt aaa ata aac	545	550	555	1680
Glu Ala Thr Gly Ile Phe Lys Lys Leu Pro Gln Leu Arg Lys Ile Asn				
ttt agc aac aat aag atc aca gat att gag gag gga gca ttt gaa gga	560	565	570	1728
Phe Ser Asn Asn Lys Ile Thr Asp Ile Glu Glu Gly Ala Phe Glu Gly				
gca tct ggt gta aat gaa ata ctt ctt acg agt aat cgt ttg gaa aat	580	585	590	1776
Ala Ser Gly Val Asn Glu Ile Leu Leu Thr Ser Asn Arg Leu Glu Asn				
gtg cag cat aag atg ttc aag gga ttg gaa agc ctc aaa act ttg atg	595	600	605	1824
Val Gln His Lys Met Phe Lys Gly Leu Glu Ser Leu Lys Thr Leu Met				
ttg aga agc aat cga ata acc ttt gac agt ttc ata gga	610	615	620	1872
Leu Arg Ser Asn Arg Ile Thr Cys Val Gly Asn Asp Ser Phe Ile Gly				
ctc agt tct gtg cgt ttg ctt tct ttg tat gat aat caa att act aca	625	630	635	1920
Leu Ser Ser Val Arg Leu Leu Ser Leu Tyr Asp Asn Gln Ile Thr Thr				
gtt gca cca ggg gca ttt gat act ctc cat tct tta tct act cta aac	640	645	650	1968
Val Ala Pro Gly Ala Phe Asp Thr Leu His Ser Leu Ser Thr Leu Asn				
ctc ttg gcc aat cct ttt aac tgt aac tgc tac ctg gct tgg ttg gga	660	665	670	2016
Leu Leu Ala Asn Pro Phe Asn Cys Asn Cys Tyr Leu Ala Trp Leu Gly				
gag tgg ctg aga aag aag aga att gtc acg gga aat cct aga tgt caa	675	680	685	2064
Glu Trp Leu Arg Lys Lys Arg Ile Val Thr Gly Asn Pro Arg Cys Gln				
aaa cca tac ttc ctg aaa gaa ata ccc atc cag gat gtg gcc att cag	690	695	700	2112
Lys Pro Tyr Phe Leu Lys Glu Ile Pro Ile Gln Asp Val Ala Ile Gln				
gac ttc act tgt gat gac gga aat gat gac aat agt tgc tcc cca ctt	705	710	715	2160
Asp Phe Thr Cys Asp Asp Gly Asn Asp Asp Asn Ser Cys Ser Pro Leu				
tct cgc tgt cct act gaa tgt act tgc ttg gat aca gtc gtc cga tgt	720	725	730	2208
Ser Arg Cys Pro Thr Glu Cys Thr Cys Leu Asp Thr Val Val Arg Cys				
agc aac aag ggt ttg aag gtc ttg ccg aaa ggt att cca aga gat gtc	740	745	750	2256
Ser Asn Lys Gly Leu Lys Val Leu Pro Lys Gly Ile Pro Arg Asp Val				
aca gag ttg tat ctg gat gga aac caa ttt aca ctg gtt ccc aag gaa	755	760	765	2304
Thr Glu Leu Tyr Leu Asp Gly Asn Gln Phe Thr Leu Val Pro Lys Glu				
ctc tcc aac tac aaa cat tta aca ctt ata gac tta agt aac aac aga	770	775	780	2352
Leu Ser Asn Tyr Lys His Leu Thr Leu Ile Asp Leu Ser Asn Asn Arg				

ata agc acg ctt tct aat cag agc ttc agc aac atg acc cag ctc ctc	2400
Ile Ser Thr Leu Ser Asn Gln Ser Phe Ser Asn Met Thr Gln Leu Leu	
785 790 795 800	
acc tta att ctt agt tac aac cgt ctg aga tgt att cct cct cgc acc	2448
Thr Leu Ile Leu Ser Tyr Asn Arg Leu Arg Cys Ile Pro Pro Arg Thr	
805 810 815	
ttt gat gga tta aag tct ctt cga tta ctt tct cta cat gga aat gac	2496
Phe Asp Gly Leu Lys Ser Leu Arg Leu Leu Ser Leu His Gly Asn Asp	
820 825 830	
att tct gtt gtg cct gaa ggt gct ttc aat gat ctt tct gca tta tca	2544
Ile Ser Val Val Pro Glu Gly Ala Phe Asn Asp Leu Ser Ala Leu Ser	
835 840 845	
cat cta gca att gga gcc aac cct ctt tac tgt gat tgt aac atg cag	2592
His Leu Ala Ile Gly Ala Asn Pro Leu Tyr Cys Asp Cys Asn Met Gln	
850 855 860	
tgg tta tcc gac tgg gtg aag tcg gaa tat aag gag cct gga att gct	2640
Trp Leu Ser Asp Trp Val Lys Ser Glu Tyr Lys Glu Pro Gly Ile Ala	
865 870 875 880	
cgt tgt gct ggt cct gga gaa atg gca gat aaa ctt tta ctc aca act	2688
Arg Cys Ala Gly Pro Gly Glu Met Ala Asp Lys Leu Leu Leu Thr Thr	
885 890 895	
ccc tcc aaa aaa ttt acc tgt caa ggt cct gtg gat gtc aat att cta	2736
Pro Ser Lys Phe Thr Cys Gln Gly Pro Val Asp Val Asn Ile Leu	
900 905 910	
gct aag tgt aac ccc tgc cta tca aat ccg tgt aaa aat gat ggc aca	2784
Ala Lys Cys Asn Pro Cys Leu Ser Asn Pro Cys Lys Asn Asp Gly Thr	
915 920 925	
tgt aat agt gat cca gtt gac ttt tac cga tgc acc tgt cca tat ggt	2832
Cys Asn Ser Asp Pro Val Asp Phe Tyr Arg Cys Thr Cys Pro Tyr Gly	
930 935 940	
ttc aag ggg cag gac tgt gat gtc cca att cat gcc tgc atc agt aac	2880
Phe Lys Gly Gln Asp Cys Asp Val Pro Ile His Ala Cys Ile Ser Asn	
945 950 955 960	
cca tgt aaa cat gga gga act tgc cac tta aag gaa gga gaa gaa gat	2928
Pro Cys Lys His Gly Thr Cys His Leu Lys Glu Gly Glu Glu Asp	
965 970 975	
gga ttc tgg tgt att tgt gct gat gga ttt gaa gga gaa aat tgt gaa	2976
Gly Phe Trp Cys Ile Cys Ala Asp Gly Phe Glu Gly Glu Asn Cys Glu	
980 985 990	
gtc aac gtt gat gat tgt gaa gat aat gac tgt gaa aat aat tct aca	3024
Val Asn Val Asp Asp Cys Glu Asp Asn Asp Cys Glu Asn Asn Ser Thr	
995 1000 1005	
tgt gtc gat ggc att aat aac tac aca tgc ctt tgc cca cct gag tat	3072
Cys Val Asp Gly Ile Asn Asn Tyr Thr Cys Leu Cys Pro Pro Glu Tyr	
1010 1015 1020	
aca ggt gag ttg tgt gag gag aag ctg gac ttc tgt gcc cag gac ctg	3120
Thr Gly Glu Leu Cys Glu Glu Lys Leu Asp Phe Cys Ala Gln Asp Leu	
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Asn Pro Cys Gln His Asp Ser Lys Cys Ile Leu Thr Pro Lys Gly Phe	
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aaa tgt gac tgc aca cca ggg tac gta ggt gaa cac tgc gac atc gat	3216
Lys Cys Asp Cys Thr Pro Gly Tyr Val Gly Glu His Cys Asp Ile Asp	
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Phe Asp Asp Cys Gln Asp Asn Lys Cys Lys Asn Gly Ala His Cys Thr	
1075 1080 1085	

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Asp Ala Val Asn Gly Tyr Thr Cys Ile Cys Pro Glu Gly Tyr Ser Gly	
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Cys Asp Asn Phe Asp Cys Gln Asn Gly Ala Gln Cys Ile Val Arg Ile	
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aat gag cca ata tgt cag tgt ttg cct ggc tat cag gga gaa aag tgt	3456
Asn Glu Pro Ile Cys Gln Cys Leu Pro Gly Tyr Gln Gly Glu Lys Cys	
1140 1145 1150	
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Glu Lys Leu Val Ser Val Asn Phe Ile Asn Lys Glu Ser Tyr Leu Gln	
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Ile Pro Ser Ala Lys Val Arg Pro Gln Thr Asn Ile Thr Leu Gln Ile	
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gcc aca gat gaa gac agc gga atc ctc ctg tat aag ggt gac aaa gac	3600
Ala Thr Asp Glu Asp Ser Gly Ile Leu Leu Tyr Lys Gly Asp Lys Asp	
1185 1190 1195 1200	
cat atc gcg gta gaa ctc tat cgg ggg cgt gtt cgt gcc agc tat gac	3648
His Ile Ala Val Glu Leu Tyr Arg Gly Arg Val Arg Ala Ser Tyr Asp	
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acc ggc tct cat cca gct tct gcc att tac agt gtg gag aca atc aat	3696
Thr Gly Ser His Pro Ala Ser Ala Ile Tyr Ser Val Glu Thr Ile Asn	
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gat gga aac ttc cac att gtg gaa cta ctt gcc ttg gat cag agt ctc	3744
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Ser Leu Ser Val Asp Gly Gly Asn Pro Lys Ile Ile Thr Asn Leu Ser	
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Lys Gln Ser Thr Leu Asn Phe Asp Ser Pro Leu Tyr Val Gly Gly Met	
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cca ggg aag agt aac gtg gca tct ctg cgc cag gcc cct ggg cag aac	3888
Pro Gly Lys Ser Asn Val Ala Ser Leu Arg Gln Ala Pro Gly Gln Asn	
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